

Human IRAK-4 protein sequence

10 20 30 40 50
MNK PIT PST YVR CLN VGL IRX LSD FID PQE GWK KLA VAI KK? SGD DRY NQF HIR

60 70 80 90 100
RFE ALL QTG KSP TSE LLF DWG TTN CTA GDL VDL LIQ NEF FAP ASL LLP DAV PKT

110 120 130 140 150 160
ANT LPS KEA ITV QKQ QMP FCD KDR TLM TPV QNL EQS YMP PDS SSP ENK SLE VSD

170 180 190 200 210
TRF HSF SFY ELK NVT NNF DER PIS VGG NKM GEG GFG VVY KGY VNN TTV AVK KLA

220 230 240 250 260 270
AMV DIT TEE LKQ QFD QEI KVM AKC QHE NLV ELL GFS SDG DDL CLV YVY MPN GSL

280 290 300 310 320
LDR LSC LDG TPP LSW HMR CKI AQG AAN GIN FLH ENH HIH RDI KSA NIL LDE AFT

330 340 350 360 370
AKI SDF GLA RAS EK? AQT VMT SRI VGT TAY MAP EAL RGE ITP KSD IYS FGV VLL

380 390 400 410 420 430
EII TGL PAV DEH REP QLL LDI KEE IED EEK TIE DYI DKX MND ADS TSV EAM YSV

440 450 460
ASQ CLH EKK NKR PDI KKV QQL LQE MTA S*

FIGURE 1

Human IRAK-4 cDNA sequence

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      10      20      30      40      50
ATG AAC AAA CCC ATA ACA CCA TCA ACA TAT GTG CGC TGC CTC AAT GTT GGA CTA
M  N  K  P  I  T  P  S  T  Y  V  R  C  L  N  V  G  L>

      60      70      80      90     100
ATT AGG AAG CTG TCA GAT TTT ATT GAT CCT CAA GAA GGA TGG AAG AAG TTA GCT
I  R  K  L  S  D  F  I  D  P  Q  E  G  W  K  K  L  A>

110      120      130      140      150      160
GTA GCT ATT AAA AAA CCA TCT GGT GAT GAT AGA TAC AAT CAG TTT CAC ATA AGG
V  A  I  K  K  P  S  G  D  D  R  Y  N  Q  F  H  I  R>

      170      180      190      200      210
AGA TTT GAA GCA TTA CTT CAA ACT GGA AAA AGT CCC ACT TCT GAA TTA CTG TTT
R  F  E  A  L  L  Q  T  G  K  S  P  T  S  E  L  L  F>

      220      230      240      250      260      270
GAC TGG GGC ACC ACA AAT TGC ACA GCT GGT GAT CTT GTG GAT CTT TTG ATC CAA
D  W  G  T  T  N  C  T  A  G  D  L  V  D  L  L  I  Q>

      280      290      300      310      320
AAT GAA TTT TTT GCT CCT GCG AGT CTT TTG CTC CCA GAT GCT GTT CCC AAA ACT
N  E  F  F  A  P  A  S  L  L  L  P  D  A  V  P  K  T>

      330      340      350      360      370
GCT AAT ACA CTA CCT TCT AAA GAA GCT ATA ACA GTT CAG CAA AAA CAG ATG CCT
A  N  T  L  P  S  K  E  A  I  T  V  Q  Q  K  Q  M  P>

380      390      400      410      420      430
TTC TGT GAC AAA GAC AGG ACA TTG ATG ACA CCT GTG CAG AAT CTT GAA CAA AGC
F  C  D  K  D  R  T  L  M  T  P  V  Q  N  L  E  Q  S>

      440      450      460      470      480
TAT ATG CCA CCT GAC TCC TCA AGT CCA GAA AAT AAA AGT TTA GAA GTT AGT GAT
Y  M  P  P  D  S  S  S  P  E  N  K  S  L  E  V  S  D>

      490      500      510      520      530      540
ACA CGT TTT CAC AGT TTT TCA TTT TAT GAA TTG AAG AAT GTC ACA AAT AAC TTT
T  R  F  H  S  F  S  F  Y  E  L  K  N  V  T  N  N  F>

      550      560      570      580      590
GAT GAA CGA CCC ATT TCT GTT GGT GGT AAT AAA ATG GGA GAG GGA GGA TTT GGA
D  E  R  P  I  S  V  G  G  N  K  M  G  E  G  G  F  G>

      600      610      620      630      640

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FIGURE 2A

GTT GTA TAT AAA GGC TAC GTA AAT AAC ACA ACT GTG GCA GTG AAG AAG CTT GCA
V V Y K G Y V N N T T V A V K K L A>

650 660 670 680 690 700
GCA ATG GTT GAC ATT ACT ACT GAA GAA CTG AAA CAG CAG TTT GAT CAA GAA ATA
A M V D I T T E E L K Q Q F D Q E I>

710 720 730 740 750
AAA GTA ATG GCA AAG TGT CAA CAT GAA AAC TTA GTA GAA CTA CTT GGT TTC TCA
K V M A K C Q H E N L V E L L G F S>

760 770 780 790 800 810
AGT GAT GGA GAT GAC CTC TGC TTA GTA TAT GTT TAC ATG CCT AAT GGT TCA TTG
S D G D D L C L V Y V Y M P N G S L>

820 830 840 850 860
CTA GAC AGA CTC TCT TGC TTG GAT GGT ACT CCA CCA CTT TCT TGG CAC ATG AGA
L D R L S C L D G T P P L S W H M R>

870 880 890 900 910
TGC AAG ATT GCT CAG GGT GCA GCT AAT GGC ATC AAT TTT CTA CAT GAA AAT CAT
C K I A Q G A A N G I N F L H E N H>

920 930 940 950 960 970
CAT ATT CAT AGA GAT ATT AAA AGT GCA AAT ATC TTA CTG GAT GAA GCT TTT ACT
H I H R D I K S A N I L L D E A F T>

980 990 1000 1010 1020
GCT AAA ATA TCT GAC TTT GGC CTT GCA CGG GCT TCT GAG AAG TTT GCC CAG ACA
A K I S D F G L A R A S E K F A Q T>

1030 1040 1050 1060 1070 1080
GTC ATG ACT AGC AGA ATT GTG GGA ACA ACA GCT TAT ATG GCA CCA GAA GCT TTG
V M T S R I V G T T A Y M A P E A L>

1090 1100 1110 1120 1130
CGT GGA GAA ATA ACA CCC AAA TCT GAT ATT TAC AGC TTT GGT GTG GTT TTA CTA
R G E I T P K S D I Y S F G V V L L>

1140 1150 1160 1170 1180
GAA ATA ATA ACT GGA CTT CCA GCT GTG GAT GAA CAC CGT GAA CCT CAG TTA TTG
E I I T G L P A V D E H R E P Q L L>

1190 1200 1210 1220 1230 1240
CTA GAT ATT AAA GAA GAA ATT GAA GAT GAA GAA AAG ACA ATT GAA GAT TAT ATT
L D I K E E I E D E E K T I E D Y I>

FIGURE 2B

1250 1260 1270 1280 1290
 GAT AAA AAG ATG AAT GAT GCT GAT TCC ACT TCA GTT GAA GCT ATG TAC TCT GTT
 D K K M N D A D S T S V E A M Y S V>

 1300 1310 1320 1330 1340 1350
 GCT AGT CAA TGT CTG CAT GAA AAG AAA AAT AAG AGA CCA GAC ATT AAG AAG GTT
 A S Q C L H E K K N K R P D I K K V>

 1360 1370 1380
 CAA CAG CTG CTG CAA GAG ATG ACA GCT TCT TAA
 Q Q L L Q E M T A S *>

FIGURE 2C

mIRAK-4 amino acid sequence

10	20	30	40	50	
MNK	PLT	PST	YIR	NLN	VGI LRK LSD FID PQE GWK KLA VAI KKP SGD DRY NQF HIR
60	70	80	90	100	
RFE	ALL	QTG	KSP	TCE	LLF DWG TTN CTV GDL VDL LVQ IEL FAP ATL LLP DAV PQT
110	120	130	140	150	160
VKS	LPP	REA	ATV	AQT	HGP CQE KDR TSV MPM PKL EHS CEP PDS SSP DNR SVE SSD
170	180	190	200	210	
TRF	HSF	SFH	ELK	SIT	NNF DEQ PAS AGG NRM GEG GFG VVY KGC VNN TIV AVK KLG
220	230	240	250	260	270
AMV	EIS	TEE	LKQ	QFD	QEI KVM ATC QHE NLV ELL GFS SDS DNL CLV YAY MPN GSL
280	290	300	310	320	
LDR	LSC	LDG	TPP	LSW	HTR CKV AQG TAN GIR FLH ENH HIH RDI KSA NIL LDK DFT
330	340	350	360	370	
AKI	SDF	GLA	RAS	ARL	AQT VMT SRI VGT TAY MAP EAL RGE ITP KSD IYS FGV VLL
380	390	400	410	420	430
ELI	TGL	AAV	DEN	REP	QLL LDI KEE IED EEK TIE DYT DEX MSD ADP ASV EAM YSA
440	450	460			
ASQ	CLH	EKK	NRR	PDI	AKV QQL LQE MSA *

FIGURE 3

mIRAK-4 nucleotide sequence:

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      10      20      30      40      50
GCG GCC GCG TCG ACA TGC CCC GGT GAC CCG CAG CAT CCC GAT CGC AGG CAG TCT

      60      70      80      90     100
GAA GTC GCC TGG TGG TCC TGC GTC CTC CAC CCC CGA GTC CTC GCC GGA CGT GGC

110      120      130      140      150      160
GGG ACG CCG ATC GCC TTG TCC AGG AAG CGA GGG ACG TCC GAG AGG AAG TAG AAG

      170      180      190      200      210
ATG AAC AAG CCG TTG ACA CCA TCG ACA TAC ATA CGC AAC CTT AAT GTG GGG ATC
M  N  K  P  L  T  P  S  T  Y  I  R  N  L  N  V  G  I>

      220      230      240      250      260      270
CTT AGG AAG CTG TCG GAT TTT ATT GAT CCT CAA GAA GGG TGG AAG AAA TTA GCA
L  R  K  L  S  D  F  I  D  P  Q  E  G  W  K  K  L  A>

      280      290      300      310      320
GTA GCT ATC AAA AAG CCG TCC GGC GAC GAC AGA TAC AAT CAG TTC CAT ATA AGG
V  A  I  K  K  P  S  G  D  D  R  Y  N  Q  F  H  I  R>

      330      340      350      360      370
AGA TTC GAA GCC TTA CTT CAG ACC GGG AAG AGC CCC ACC TGT GAA CTG CTG TTT
R  F  E  A  L  L  Q  T  G  K  S  P  T  C  E  L  L  F>

380      390      400      410      420      430
GAC TGG GGC ACC ACG AAC TGC ACA GTT GGC GAC CTT GTG GAT CTA CTG GTC CAG
D  W  G  T  T  N  C  T  V  G  D  L  V  D  L  L  V  Q>

      440      450      460      470      480
ATT GAG CTG TTT GCC CCC GCC ACT CTC CTG CTG CCG GAT GCC GTT CCC CAA ACC
I  E  L  F  A  P  A  T  L  L  L  P  D  A  V  P  Q  T>

      490      500      510      520      530      540
GTC AAA AGC CTG CCT CCT AGA GAA GCG GCA ACA GTG GCA CAA ACA CAC GGG CCT
V  K  S  L  P  P  R  E  A  A  T  V  A  Q  T  H  G  P>

      550      560      570      580      590
TGT CAG GAA AAG GAC AGG ACA TCC GTA ATG CCT ATG CCG AAG CTA GAA CAC AGC
C  Q  E  K  D  R  T  S  V  M  P  M  P  K  L  E  H  S>

      600      610      620      630      640
TGC GAG CCA CCG GAC TCC TCA AGC CCA GAC AAC AGA AGT GTA GAG TCC AGC GAC
C  E  P  P  D  S  S  S  P  D  N  R  S  V  E  S  S  D>

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FIGURE 4A

650 660 670 680 690 700
 ACT CGG TTC CAC AGC TTC TCG TTC CAT GAA CTG AAG AGC ATC ACA AAC AAC TTC
 T R F H S F S F H E L K S I T N N F>

710 720 730 740 750
 GAC GAG CAA CCC GCG TCT GCC GGT GGC AAC CGG ATG GGA GAG GGG GGA TTT GGA
 D E Q P A S A G G N R M G E G G F G>

760 770 780 790 800 810
 GTG GTG TAC AAG GGC TGT GTG AAC AAC ACC ATC GTG GCG GTG AAG AAG CTC GGA
 V V Y K G C V N N T I V A V K K L G>

820 830 840 850 860
 GCG ATG GTT GAA ATC AGT ACT GAA GAA CTA AAG CAA CAG TTT GAT CAA GAA ATT
 A M V E I S T E E L K Q Q F D Q E I>

870 880 890 900 910
 AAA GTA ATG GCA ACG TGT CAG CAC GAG AAC CTG GTG GAG CTG CTC GGC TTC TCC
 K V M A T C Q H E N L V E L L G F S>

920 930 940 950 960 970
 AGC GAC AGC GAC AAC CTG TGC TTA GTG TAT GCT TAC ATG CCC AAC GGG TCC TTG
 S D S D N L C L V Y A Y M P N G S L>

980 990 1000 1010 1020
 CTG GAC AGA CTG TCC TGC CTG GAT GGT ACA CCA CCG CTT TCC TGG CAC ACA AGG
 L D R L S C L D G T P P L S W H T R>

1030 1040 1050 1060 1070 1080
 TGC AAG GTT GCT CAG GGG ACA GCA AAT GGC ATC AGG TTT CTG CAT GAA AAT CAT
 C K V A Q G T A N G I R F L H E N H>

1090 1100 1110 1120 1130
 CAC ATT CAT AGA GAT ATT AAA AGT GCA AAT ATC TTA CTA GAC AAA GAC TTT ACT
 H I H R D I K S A N I L L D K D F T>

1140 1150 1160 1170 1180
 GCC AAA ATA TCT GAC TTT GGG CTT GCA CGG GCT TCG GCA AGG CTA GCG CAG ACG
 A K I S D F G L A R A S A R L A Q T>

1190 1200 1210 1220 1230 1240
 GTC ATG ACC AGC CGA ATC GTG GGC ACA ACG GCT TAC ATG GCA CCC GAA GCT TTG
 V M T S R I V G T T A Y M A P E A L>

1250 1260 1270 1280 1290
 CGG GGA GAA ATA ACA CCC AAA TCT GAC ATC TAC AGC TTC GGC GTG GTT CTG TTG
 R G E I T P K S D I Y S F G V V L L>

FIGURE 4B

1300 1310 1320 1330 1340 1350
 GAG CTG ATA ACC GGG CTG GCG GCT GTG GAT GAA AAC CGT GAA CCT CAA CTA CTG
 E L I T G L A A V D E N R E P Q L L>

1360 1370 1380 1390 1400
 CTG GAT ATT AAA GAA GAG ATT GAA GAT GAA GAG AAG ACG ATT GAA GAT TAC ACG
 L D I K E E I E D E E K T I E D Y T>

1410 1420 1430 1440 1450
 GAT GAG AAG ATG AGC GAT GCG GAC CCT GCT TCG GTG GAA GCA ATG TAC TCT GCT
 D E K M S D A D P A S V E A M Y S A>

1460 1470 1480 1490 1500 1510
 GCT AGC CAG TGT CTG CAT GAG AAG AAA AAC AGA CGG CCA GAC ATT GCA AAG GTT
 A S Q C L H E K K N R R P D I A K V>

1520 1530 1540
 CAA CAG CTG CTA CAA GAG ATG TCT GCT TAA
 Q Q L L Q E M S A *>

FIGURE 4C

[illegible]